j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19.

2. (Amended) A [Polypeptide] polypeptide according to Claim 1, [characterized in that it] [comprises] comprising [the] an amino acid sequence selected from the group consisting of SEQ ID No. 6, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 and SEQ ID No. 19.

3. (Amended) A [Polypeptide] polypeptide according to Claim 1, [characterized in that it comprises] comprising [the] a sequence lying between:

- residue 110 and residue 310 of SEQ ID No. 2 or 6;
- residue 60 and residue 260 of SEQ ID No. 8.

4. (Amended) A [Polypeptide] polypeptide according to Claim 1, [characterized in that it] which [results] is produced from an alternative splicing of [the] messenger RNA of [the] a corresponding gene.

5. (Amended) A [Polypeptide] polypeptide according to [any one of the preceding claims,] Claim 1 [characterized in that it] that is a recombinant polypeptide produced in the form of a fusion protein.

6. (Amended) An [Isolated] isolated nucleic acid sequence coding for a polypeptide according to [any one of the preceding claims] Claim 1.

7. (Amended) An [Isolated] isolated nucleic acid sequence according to Claim 6, [characterized in that it is] said nucleic acid having a sequence selected from the group consisting of:

a) [the] sequence SEQ ID No. 1;

b) [the] sequence SEQ ID No. 3;

c) [the] sequence SEQ ID No. 5;

d) [the] sequence SEQ ID No. 7;

e) [the] sequence SEQ ID No. 9;

f) [the] sequence SEQ ID No. 11;

g) [the] sequence SEQ ID No. 12;

h) [the] sequence SEQ ID No. 14;

i) [the] sequence SEQ ID No. 16;

j) [the] sequence SEQ ID No. 18;

k)[the] nucleic acid sequences capable of hybridizing specifically with [the] sequence SEQ ID No. 1, SEQ ID No. 3, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 12, SEQ ID No. 14, SEQ ID No. 16 or SEQ ID No. 18 or with [the] sequences complementary to them, or of hybridizing specifically with their proximal sequences; and

l) [the] sequences derived from the sequences a), b), c), d), e), f), g), h), i), j) or k) as a result of the degeneracy of the genetic code, mutation, deletion, insertion, and alternative splicing or an allelic variability.

8. (Amended) A [Nucleotide] nucleotide sequence according to Claim 6, [characterized in that it is a sequence] selected from the group consisting of SEQ ID No. 5, SEQ ID No. 12, SEQ ID No. 14, SEQ ID No. 16 and SEQ ID No. 18 and coding, respectively, for the polypeptide of sequences SEQ ID No. 6, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 and SEQ ID No. 19.

9. (Amended) A [Cloning] cloning and/or expression vector containing a nucleic acid sequence according to [any one of Claims] Claim 6 [to 8].

10. (Amended) A [Vector] vector, according to Claim 9, [characterized in that it] which is [the] plasmid pSE1.

11. (Amended) A [Host] host cell transfected by a vector according to Claim 9 [or 10].

12. (Amended) A [Transfected] transfected host cell, according to Claim 11, [characterized in that it] which is *E. coli* MC 1061.

13. (Amended) A [Nucleotide] nucleotide probe or nucleotide primer[, characterized in that it] which hybridizes specifically with [any one of the sequences according to Claims] the nucleic acid of Claim 6 [to 8] or [the] a nucleic acid having sequences complementary to them or [the corresponding] messenger RNAs corresponding to them or [the corresponding] genes corresponding to them.

14. (Amended) A [Probe] probe or primer according to Claim 13[, characterized in] that [it] contains at least 16 nucleotides.

15. (Amended) A [Probe] probe or primer according to Claim 13 [characterized in that it] that comprises the whole of the sequence of the gene coding for [one of the polypeptides of Claim 1] a polypeptide, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19.

16.(Amended) A [Nucleotide] nucleotide probe or primer selected from the group consisting of the following oligonucleotides or sequences complementary to them:

SEQ ID No. 20: GCG AGC TGC CCT CGG AG

SEQ ID No. 21: GGT TCT GCA GGT GAC TCA G

SEQ ID No. 22: GCC ATG CCT GTC TAC AAG

SEQ ID No. 23: ACC AGC TGG TTG ACG GAG

SEQ ID No. 24: GTC AAC CAG CTG GTG GGC CAG
SEQ ID No. 25: GTG GAT CTC GGC CTC C
SEQ ID No. 26: AGG CCG GCG TGG GGA AG
SEQ ID No. 27: CTT GGC GAT CTG GCA GTA G
SEQ ID No. 28: GCG GCC ACG ACC GTG AC
SEQ ID No. 29: GGC AGC TTG GGT CTC TGG
SEQ ID No. 30: CTG TAC GTC GGT GAC CCC
SEQ ID No. 31: TCA GTG GAT CTC GGC CTC
SEQ ID No. 32: AGG GGA CGC AGC GAA ACC
SEQ ID No. 33: CCA TCA GCT CCA GGC TCT C
SEQ ID No. 34: CCA GGA CAG GCG CAG ATG
SEQ ID No. 35: GAT GAG GTG GCT GGC TGG A
SEQ ID No. 36: TGG TCA GGT TCT GCA GGT G
SEQ ID No. 37: CAC CTA CTC CAG GGA TGC
SEQ ID No. 38: AGG AAA ATA GAA GCG TCA GTC
SEQ ID No. 39: CAG GCC CAC TTG CCT GCC
and SEQ ID No. 40: CTG TCC CCA AGC TGA TGA G

17. (Amended) The [Use] use of a sequence according to [any one of Claims] Claim 6 [to 8,] for the manufacture of oligonucleotide primers for sequencing reactions or specific amplification reactions according to the PCR technique or any variant of the latter.

18. (Amended) A [Nucleotide] nucleotide primer pair[, characterized in that it comprises] comprising [the] primers selected from the group consisting of the following sequences:

a) sense primer: GCG AGC TGC CCT CGG AG (SEQ ID No. 20)
antisense primer: GGT TCT GCA GGT GAC TCA G (SEQ ID No. 21)

b) sense primer: GCC ATG CCT GTC TAC AAG (SEQ ID No. 22)
antisense primer: ACC AGC TGG TTG ACG GAG (SEQ ID No. 23)

c) sense primer: GTC AAC CAG CTG GTG GGC CAG (SEQ ID No. 24)
antisense primer: GTG GAT CTC GGC CTC C (SEQ ID No. 25)

d) sense primer: AGG CCG GCG TGG GGA AG (SEQ ID No. 26)

antisense primer: CTT GGC GAT CTG GCA GTA G (SEQ ID No. 27)

e) sense primer: GCG GCC ACG ACC GTG A (SEQ ID No. 28)
antisense primer: GGC AGC TTG GGT CTC TGG (SEQ ID No. 29)

f) sense primer: CTG TAC GTC GGT GAC CCC (SEQ ID No. 30)
antisense primer: TCA GTG GAT CTC GGC CTC (SEQ ID No. 31)

g) sense primer: AGG GGA CGC AGC GAA ACC (SEQ ID No. 32)
antisense primer: GGC AGC TTG GGT CTC TGG (SEQ ID No. 29)

h) sense primer: CCCCCCCCCCCCCCN (where N equals G, A or T)
antisense primer: CCA TCA GCT CCA GGC TCT C (SEQ ID No. 33)

i) sense primer: CCCCCCCCCCCCCCN (where N equals G, A or T)
antisense primer: CCA GGA CAG GCG CAG ATG (SEQ ID No. 34)

j) sense primer: CCCCCCCCCCCCCCCN (where N equals G, A or T)
antisense primer: CTT GGC GAT CTG GCA GTA G (SEQ ID No. 27)

k) sense primer: CAC CTA CTC CAG GGA TGC (SEQ ID No. 37)
antisense primer: AGG AAA ATA GAA GCG TCA GTC (SEQ ID No. 38) and

l) sense primer: CAG GCC CAC TTG CCT GCC (SEQ ID No. 39)
antisense primer: CTG TCC CCA AGC TGA TGA G (SEQ ID No. 40)

19. (Amended) The [Use] use of a sequence according to [any one of Claims] Claim 6 [to 8,] [which is usable] in gene therapy.

20. (Amended) The [Use] use of a sequence according to [any one of Claims] Claim 6 [to 8,] for the production of diagnostic nucleotide probes or primers, or of antisense sequences which are usable in gene therapy.

21. (Amended) The [Use] use of nucleotide primers according to [any one of Claims] Claim 6 [to 8,] for sequencing.

22. (Amended) The [Use] use of a probe or primer according to [any one of Claims] Claim 13 [to 16,] as an *in vitro* diagnostic tool for the detection, by hybridization experiments, of nucleic acid sequences coding for a polypeptide, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19 [according to any one of Claims 1 to 4,] in biological samples, or for the demonstration of aberrant syntheses or of genetic abnormalities.

23.(Amended) A [Method] method of *in vitro* diagnosis for the detection of aberrant syntheses or of genetic abnormalities in the nucleic acid sequences coding for a polypeptide, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19

[according to any one of Claims 1 to 4, characterized in that it comprises] comprising the steps of:

- [the] bringing of a nucleotide probe according to [any one of Claims] Claim 13 [to 16] into contact with a biological sample under conditions permitting the formation of a hybridization complex between the [said] probe and the [abovementioned] nucleotide sequence, where appropriate after a prior step of amplification of the [abovementioned ]nucleotide sequence;
- the detection of the hybridization complex [possibly] formed; and
- where appropriate, [the] sequencing of the hybridization complex' nucleotide sequence [forming the hybridization complex] with the probe of the invention.

24. (Amended) The [Use] use of a nucleic acid sequence according to [any one of Claims] Claim 6 [to 8,] for the production of a recombinant polypeptide wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19 [according to any one of Claims 1 to 5].

25. (Amended) A [Method] method of production of a recombinant SR-p70 protein, characterized in that transfected cells according to Claim [10 or] 11 are cultured under conditions permitting the expression of a recombinant polypeptide of sequence SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15,

SEQ ID No. 17 or SEQ ID No. 19 or any biologically active fragment or derivative, and in that the [said] recombinant polypeptide is recovered.

26. (Amended) Mono- or polyclonal antibodies or their fragments, chimeric antibodies or immunoconjugates, characterized in that they are capable of specifically recognizing a polypeptide according to [any one of Claims] Claim 1 [to 4].

27. (Amended) Use of the antibodies according to [the preceding claim,] Claim 26 for the purification or detection of a polypeptide , wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19 [according to any one of Claims 1 to 4] in a biological sample.

28. (Amended) A [Method] method of *in vitro* diagnosis of pathologies correlated with an expression or an abnormal accumulation of SR-p70 proteins, in particular the phenomena of carcinogenesis, from a biological sample, [characterized in that] comprising the steps of contacting at least one antibody according to Claim 25 [is brought into contact] with the said biological sample under conditions permitting the [possible] formation of specific immunological complexes between an SR-p70 protein and the said antibody or antibodies, and detecting the presence of [in that the] specific immunological complexes [possibly] formed [are detected].

29. (Amended) A [Kit] kit for the *in vitro* diagnosis of an expression or an abnormal accumulation of SR-p70 proteins in a biological sample and/or for measuring the level of expression of these proteins in the said sample, comprising:

- at least one antibody according to Claim 25, optionally bound to a support,
- means of visualization of the formation of specific antigen-antibody complexes between an SR-p70 protein and the said antibody, and/or means of quantification of these complexes.

30. (Amended) A [Method] method for the early diagnosis of tumour formation, [characterized in that] wherein autoantibodies directed against an SR-p70 protein are demonstrated in a serum sample drawn from an individual, according to the steps that [consist in] comprise bringing a serum sample drawn from an individual into contact with a polypeptide of the invention, optionally bound to a support, under conditions permitting the formation of specific immunological complexes between the said polypeptide and [the] autoantibodies [possibly] present in the serum sample, and in that the specific immunological complexes [possibly] formed are detected.

31. (Amended) A [Method] method of determination of an allelic variability, a mutation, a deletion, an insertion, a loss of heterozygosity or a genetic abnormality of the SR-p70 gene, characterized in that it utilizes at least one nucleotide sequence according to [any one of Claims] Claim 6 [to 8].

32. (Amended) A [Method] method of determination of an allelic variability of the SR-p70 gene at position -30 and -20 relative to the initiation ATG of exon 2 which may be involved in pathologies[, and characterized in that it comprises at least] comprising:

- a step during which exon 2 of the SR-p70 gene carrying the target sequence is amplified by PCR using a pair of oligonuclotide primers according to [any one of Claims] Claim 6 [to 8];
- a step during which the amplified products are treated with a restriction enzyme whose cleavage site corresponds to the allele sought and;

- a step during which at least one of the products of the enzyme reaction is detected or assayed.

33. (Amended) A [Pharmaceutical] pharmaceutical composition comprising an effective amount of [as active principle a] the polypeptide according to [any one of Claims] Claim 1 [to 4].

34. (Amended) A [Pharmaceutical] pharmaceutical composition according to [the preceding claim, characterized in that it comprises] Claim 33, comprising a polypeptide comprising an amino acid sequence selected from SEQ ID No. 6, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 and SEQ ID No. 19.

35. (Amended) A [Pharmaceutical] pharmaceutical composition containing an inhibitor or an activator of SR-p70 activity.

36. (Amended) A [Pharmaceutical] pharmaceutical composition containing a polypeptide derived from a polypeptide according to [any one of Claims] Claim 1 [to 5, characterized in that it] which is an inhibitor or an activator of SR-p70.

Please add the following new claims.

37. (New) The use of a probe or primer according to Claim 16 as an *in vitro* diagnostic tool for the detection, by hybridization experiments, of nucleic acid sequences coding for a polypeptide, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19 in biological samples, or for the demonstration of aberrant syntheses or of genetic abnormalities.

38. (New) A method of *in vitro* diagnosis for the detection of aberrant syntheses or of genetic abnormalities in the nucleic acid sequences coding for a polypeptide, said polypetide comprising an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any biologically active sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19

comprising the steps of:

- bringing of a nucleotide probe according to Claim 16 into contact with a biological sample under conditions permitting the formation of a hybridization complex between the probe and the nucleotide sequence, where appropriate, after a prior step of amplification of the nucleotide sequence;
- the detection of the hybridization complex formed; and
- where appropriate, sequencing of the hybridization complex' nucleotide sequence with the probe of the invention.